

## SEQUENCE LISTING

<110> DIDEBERG, OTTO  
VERNET, THIERRY  
MOUZ, NICOLAS

<120> STREPTOCOCCUS PNEUMONIAE PBP2X MINI-PROTEIN AND USES  
THEREOF

<130> 70457-19

<140> 10/520,655

<141> 2005-03-07

<150> PCT/IB03/003397

<151> 2003-07-11

<150> FR 02/08724

<151> 2002-07-11

<160> 18

<170> PatentIn Ver. 3.3

<210> 1

<211> 551

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
mini-PBP2x construct

<400> 1

Gly Ser Gly Ala Lys Arg Gly Thr Ile Tyr Asp Arg Asn Gly Val Pro  
1 5 10 15

Ile Ala Glu Asp Ala Thr Ser Gly Gly Pro Asn Arg Ser Tyr Pro Asn  
20 25 30

Gly Gln Phe Ala Ser Ser Phe Ile Gly Gly Gly Met Glu Ser Ser Leu  
35 40 45

Asn Ser Ile Leu Ala Gly Gly Gly Gly Asp Gly Lys Asp Val Tyr Thr  
50 55 60

Thr Ile Ser Ser Pro Leu Gln Ser Phe Met Glu Thr Gln Met Asp Ala  
65 70 75 80

Phe Gln Glu Lys Val Lys Gly Lys Tyr Met Thr Ala Thr Leu Val Ser  
85 90 95

Ala Lys Thr Gly Glu Ile Leu Ala Thr Thr Gln Arg Pro Thr Phe Asp  
100 105 110

Ala Asp Thr Lys Glu Gly Ile Thr Glu Asp Phe Val Trp Arg Asp Ile  
115 120 125



Leu	Tyr	Gln	Ser	Asn	Tyr	Glu	Pro	Gly	Ser	Thr	Met	Lys	Val	Met	Met	130	135	140
Leu	Ala	Ala	Ala	Ile	Asp	Asn	Asn	Thr	Phe	Pro	Gly	Gly	Glu	Val	Phe	145	150	155
Asn	Ser	Ser	Glu	Leu	Lys	Ile	Ala	Asp	Ala	Thr	Ile	Arg	Asp	Trp	Asp	165	170	175
Val	Asn	Glu	Gly	Leu	Thr	Gly	Gly	Arg	Met	Met	Thr	Phe	Ser	Gln	Gly	180	185	190
Phe	Ala	His	Ser	Ser	Asn	Val	Gly	Met	Thr	Leu	Leu	Glu	Gln	Lys	Met	195	200	205
Gly	Asp	Ala	Thr	Trp	Leu	Asp	Tyr	Leu	Asn	Arg	Phe	Lys	Phe	Gly	Val	210	215	220
Pro	Thr	Arg	Phe	Gly	Leu	Thr	Asp	Glu	Tyr	Ala	Gly	Gln	Leu	Pro	Ala	225	230	235
Asp	Asn	Ile	Val	Asn	Ile	Ala	Gln	Ser	Ser	Phe	Gly	Gln	Gly	Ile	Ser	245	250	255
Val	Thr	Gln	Thr	Gln	Met	Ile	Arg	Ala	Phe	Thr	Ala	Ile	Ala	Asn	Asp	260	265	270
Gly	Val	Met	Leu	Glu	Pro	Lys	Phe	Ile	Ser	Ala	Ile	Tyr	Asp	Pro	Asn	275	280	285
Asp	Gln	Thr	Ala	Arg	Lys	Ser	Gln	Lys	Glu	Ile	Val	Gly	Asn	Pro	Val	290	295	300
Ser	Lys	Asp	Ala	Ala	Ser	Leu	Thr	Arg	Thr	Asn	Met	Val	Leu	Val	Gly	305	310	315
Thr	Asp	Pro	Val	Tyr	Gly	Thr	Met	Tyr	Asn	His	Ser	Thr	Gly	Lys	Pro	325	330	335
Thr	Val	Thr	Val	Pro	Gly	Gln	Asn	Val	Ala	Leu	Lys	Ser	Gly	Thr	Ala	340	345	350
Gln	Ile	Ala	Asp	Glu	Lys	Asn	Gly	Gly	Tyr	Leu	Val	Gly	Leu	Thr	Asp	355	360	365
Tyr	Ile	Phe	Ser	Ala	Val	Ser	Met	Ser	Pro	Ala	Glu	Asn	Pro	Asp	Phe	370	375	380
Ile	Leu	Tyr	Val	Thr	Val	Gln	Gln	Pro	Glu	His	Tyr	Ser	Gly	Ile	Gln	385	390	395
Leu	Gly	Glu	Phe	Ala	Asn	Pro	Ile	Leu	Glu	Arg	Ala	Ser	Ala	Met	Lys	405	410	415
Asp	Ser	Leu	Asn	Leu	Gln	Thr	Thr	Ala	Lys	Ala	Leu	Glu	Gln	Val	Ser	420	425	430

Gln Gln Ser Pro Tyr Pro Met Pro Ser Val Lys Asp Ile Ser Pro Gly  
           435                          440                          445  
 Asp Leu Ala Glu Glu Leu Arg Arg Asn Leu Val Gln Pro Ile Val Val  
           450                          455                          460  
 Gly Thr Gly Thr Lys Ile Lys Asn Ser Ser Ala Glu Glu Gly Lys Asn  
           465                          470                          475                          480  
 Leu Ala Pro Asn Gln Gln Val Leu Ile Leu Ser Asp Lys Ala Glu Glu  
                           485                          490                          495  
 Val Pro Asp Met Tyr Gly Trp Thr Lys Glu Thr Ala Glu Thr Leu Ala  
                           500                          505                          510  
 Lys Trp Leu Asn Ile Glu Leu Glu Phe Gln Gly Ser Gly Ser Thr Val  
           515                          520                          525  
 Gln Lys Gln Asp Val Arg Ala Asn Thr Ala Ile Lys Asp Ile Lys Lys  
           530                          535                          540  
 Ile Thr Leu Thr Leu Gly Asp  
           545                          550

<210> 2  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           primer

<400> 2  
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<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           primer

<400> 3  
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<210> 4  
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 <212> DNA  
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<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4

cataaatagt cccacgtttg gccccggatc cacgcggaac cag

43

<210> 5

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

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gtttgggtaa ctacgattgg gacctccaga ggttgcattc tcagcaatcg g

51

<210> 6

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 6

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48

<210> 7

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 7

tgtataaaca tccttaccgt cccacctcc ccctgcaaga atactgttc

49

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 8

ccgcatatgg ccaaactgg gactatztat

30

<210> 9  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 9  
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32

<210> 10  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 peptide

<220>  
 <221> MOD\_RES  
 <222> (3)  
 <223> variable amino acid

<220>  
 <221> MOD\_RES  
 <222> (4)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (5)  
 <223> variable amino acid

<220>  
 <221> MOD\_RES  
 <222> (6)  
 <223> Asp or Ser

<220>  
 <221> MOD\_RES  
 <222> (10)..(12)  
 <223> variable amino acid

<400> 10  
 Arg Gly Xaa Xaa Xaa Xaa Arg Ser Gly Xaa Xaa Xaa Ala  
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<210> 11  
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<220>  
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<220>  
 <221> MOD\_RES  
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 <223> Arg or Lys

<220>  
 <221> MOD\_RES  
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 <223> variable amino acid

<220>  
 <221> MOD\_RES  
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<400> 11  
 Xaa Xaa Xaa Pro Xaa Gly  
       1                  5

<210> 12  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<220>  
 <221> MOD\_RES  
 <222> (1)  
 <223> Gly or Tyr

<220>  
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 <221> MOD\_RES  
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 <223> variable amino acid

<220>  
 <221> MOD\_RES  
 <222> (8)..(9)  
 <223> variable amino acid

<400> 12  
 Xaa Xaa Glu Xaa Xaa Asp Xaa Xaa Leu  
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<210> 13  
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<220>  
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<220>  
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 <223> hydrophobic amino acid

<220>  
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<400> 13  
 Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Gln  
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<210> 14  
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<220>  
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 <223> Gly or Ser

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<220>  
 <221> MOD\_RES  
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 <223> variable amino acid

<220>  
 <221> MOD\_RES  
 <222> (13)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (14)  
 <223> Asp or Asn

<400> 14  
 Thr Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Ser Pro Xaa Xaa Xaa  
           1                          5                          10

<210> 15  
 <211> 8  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<220>  
 <221> MOD\_RES  
 <222> (1)  
 <223> hydrophobic amino acid

<220>  
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 <222> (4)  
 <223> Ala or Gly

<220>  
 <221> MOD\_RES  
 <222> (6)..(7)  
 <223> variable amino acid

<400> 15  
 Xaa Glu Pro Xaa Ser Xaa Xaa Lys  
           1                          5



<210> 16  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<220>  
 <221> MOD\_RES  
 <222> (1)  
 <223> hydrophobic amino acid

<220>  
 <221> MOD\_RES  
 <222> (2)..(3)  
 <223> variable amino acid

<220>  
 <221> MOD\_RES  
 <222> (5)  
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<220>  
 <221> MOD\_RES  
 <222> (7)  
 <223> hydrophobic amino acid

<400> 16  
 Xaa Xaa Xaa Ser Xaa Asn Xaa  
     1                    5

<210> 17  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 17  
 Ala Lys Arg Gly Thr Ile Tyr  
     1                    5

<210> 18  
 <211> 750  
 <212> PRT  
 <213> Streptococcus pneumoniae

<400> 18  
 Met Lys Trp Thr Lys Arg Val Ile Arg Tyr Ala Thr Lys Asn Arg Lys  
     1                    5                    10                    15

Ser	Pro	Ala	Glu	Asn	Arg	Arg	Arg	Val	Gly	Lys	Ser	Leu	Ser	Leu	Leu	20	25	30	
Ser	Val	Phe	Val	Phe	Ala	Ile	Phe	Leu	Val	Asn	Phe	Ala	Val	Ile	Ile	35	40	45	
Gly	Thr	Gly	Thr	Arg	Phe	Gly	Thr	Asp	Leu	Ala	Lys	Glu	Ala	Lys	Lys	50	55	60	
Val	His	Gln	Thr	Thr	Arg	Thr	Val	Pro	Ala	Lys	Arg	Gly	Thr	Ile	Tyr	65	70	75	80
Asp	Arg	Asn	Gly	Val	Pro	Ile	Ala	Glu	Asp	Ala	Thr	Ser	Tyr	Asn	Val	85	90	95	
Tyr	Ala	Val	Ile	Asp	Glu	Asn	Tyr	Lys	Ser	Ala	Thr	Gly	Lys	Ile	Leu	100	105	110	
Tyr	Val	Glu	Lys	Thr	Gln	Phe	Asn	Lys	Val	Ala	Glu	Val	Phe	His	Lys	115	120	125	
Tyr	Leu	Asp	Met	Glu	Glu	Ser	Tyr	Val	Arg	Glu	Gln	Leu	Ser	Gln	Pro	130	135	140	
Asn	Leu	Lys	Gln	Val	Ser	Phe	Gly	Ala	Lys	Gly	Asn	Gly	Ile	Thr	Tyr	145	150	155	160
Ala	Asn	Met	Met	Ser	Ile	Lys	Lys	Glu	Leu	Glu	Ala	Ala	Glu	Val	Lys	165	170	175	
Gly	Ile	Asp	Phe	Thr	Thr	Ser	Pro	Asn	Arg	Ser	Tyr	Pro	Asn	Gly	Gln	180	185	190	
Phe	Ala	Ser	Ser	Phe	Ile	Gly	Leu	Ala	Gln	Leu	His	Glu	Asn	Glu	Asp	195	200	205	
Gly	Ser	Lys	Ser	Leu	Leu	Gly	Thr	Ser	Gly	Met	Glu	Ser	Ser	Leu	Asn	210	215	220	
Ser	Ile	Leu	Ala	Gly	Thr	Asp	Gly	Ile	Ile	Thr	Tyr	Glu	Lys	Asp	Arg	225	230	235	240
Leu	Gly	Asn	Ile	Val	Pro	Gly	Thr	Glu	Gln	Val	Ser	Gln	Arg	Thr	Met	245	250	255	
Asp	Gly	Lys	Asp	Val	Tyr	Thr	Thr	Ile	Ser	Ser	Pro	Leu	Gln	Ser	Phe	260	265	270	
Met	Glu	Thr	Gln	Met	Asp	Ala	Phe	Gln	Glu	Lys	Val	Lys	Gly	Lys	Tyr	275	280	285	
Met	Thr	Ala	Thr	Leu	Val	Ser	Ala	Lys	Thr	Gly	Glu	Ile	Leu	Ala	Thr	290	295	300	
Thr	Gln	Arg	Pro	Thr	Phe	Asp	Ala	Asp	Thr	Lys	Glu	Gly	Ile	Thr	Glu	305	310	315	320

Asp Phe Val Trp Arg Asp Ile Leu Tyr Gln Ser Asn Tyr Glu Pro Gly  
 325 330 335  
 Ser Thr Met Lys Val Met Met Leu Ala Ala Ala Ile Asp Asn Asn Thr  
 340 345 350  
 Phe Pro Gly Gly Glu Val Phe Asn Ser Ser Glu Leu Lys Ile Ala Asp  
 355 360 365  
 Ala Thr Ile Arg Asp Trp Asp Val Asn Glu Gly Leu Thr Gly Gly Arg  
 370 375 380  
 Met Met Thr Phe Ser Gln Gly Phe Ala His Ser Ser Asn Val Gly Met  
 385 390 395 400  
 Thr Leu Leu Glu Gln Lys Met Gly Asp Ala Thr Trp Leu Asp Tyr Leu  
 405 410 415  
 Asn Arg Phe Lys Phe Gly Val Pro Thr Arg Phe Gly Leu Thr Asp Glu  
 420 425 430  
 Tyr Ala Gly Gln Leu Pro Ala Asp Asn Ile Val Asn Ile Ala Gln Ser  
 435 440 445  
 Ser Phe Gly Gln Gly Ile Ser Val Thr Gln Thr Gln Met Ile Arg Ala  
 450 455 460  
 Phe Thr Ala Ile Ala Asn Asp Gly Val Met Leu Glu Pro Lys Phe Ile  
 465 470 475 480  
 Ser Ala Ile Tyr Asp Pro Asn Asp Gln Thr Ala Arg Lys Ser Gln Lys  
 485 490 495  
 Glu Ile Val Gly Asn Pro Val Ser Lys Asp Ala Ala Ser Leu Thr Arg  
 500 505 510  
 Thr Asn Met Val Leu Val Gly Thr Asp Pro Val Tyr Gly Thr Met Tyr  
 515 520 525  
 Asn His Ser Thr Gly Lys Pro Thr Val Thr Val Pro Gly Gln Asn Val  
 530 535 540  
 Ala Leu Lys Ser Gly Thr Ala Gln Ile Ala Asp Glu Lys Asn Gly Gly  
 545 550 555 560  
 Tyr Leu Val Gly Leu Thr Asp Tyr Ile Phe Ser Ala Val Ser Met Ser  
 565 570 575  
 Pro Ala Glu Asn Pro Asp Phe Ile Leu Tyr Val Thr Val Gln Gln Pro  
 580 585 590  
 Glu His Tyr Ser Gly Ile Gln Leu Gly Glu Phe Ala Asn Pro Ile Leu  
 595 600 605  
 Glu Arg Ala Ser Ala Met Lys Asp Ser Leu Asn Leu Gln Thr Thr Ala  
 610 615 620

Lys	Ala	Leu	Glu	Gln	Val	Ser	Gln	Gln	Ser	Pro	Tyr	Pro	Met	Pro	Ser
625					630					635					640
Val	Lys	Asp	Ile	Ser	Pro	Gly	Asp	Leu	Ala	Glu	Glu	Leu	Arg	Arg	Asn
				645					650						655
Leu	Val	Gln	Pro	Ile	Val	Val	Gly	Thr	Gly	Thr	Lys	Ile	Lys	Asn	Ser
			660					665						670	
Ser	Ala	Glu	Glu	Gly	Lys	Asn	Leu	Ala	Pro	Asn	Gln	Gln	Val	Leu	Ile
		675					680								
Leu	Ser	Asp	Lys	Ala	Glu	Glu	Val	Pro	Asp	Met	Tyr	Gly	Trp	Thr	Lys
	690						695				700				
Glu	Thr	Ala	Glu	Thr	Leu	Ala	Lys	Trp	Leu	Asn	Ile	Glu	Leu	Glu	Phe
705					710					715					720
Gln	Gly	Ser	Gly	Ser	Thr	Val	Gln	Lys	Gln	Asp	Val	Arg	Ala	Asn	Thr
				725					730					735	
Ala	Ile	Lys	Asp	Ile	Lys	Lys	Ile	Thr	Leu	Thr	Leu	Gly	Asp		
			740					745					750		